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'Eisenbergiella massiliensis', a new species isolated from human stool collected after bariatric surgery

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Abstract

We report the principal characteristics of '*Eisenbergiella massiliensis*' sp. nov. strain AT11 (CSURP = P2120, DSM = 101499) that was isolated from a stool sample collected after bariatric surgery of a 56-year-old obese French woman.

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Keywords: Culturomics, *Eisenbergiella massiliensis*, human gastrointestinal microbiome, obesity, taxonomy

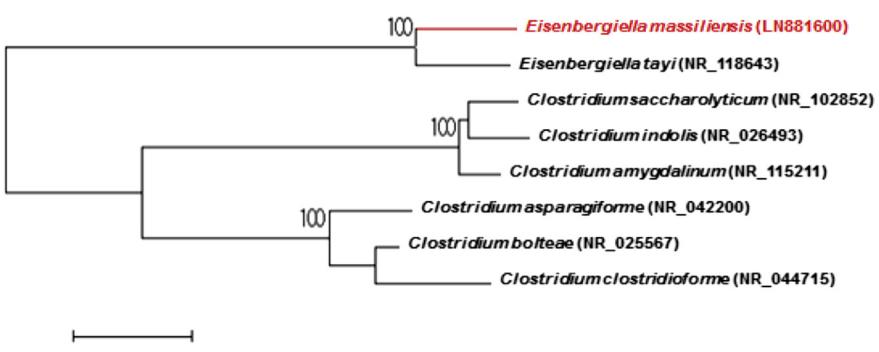
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In April 2011, as part of a culturomics study [1,2] to explore the gut microbiota from obese patients before and after bariatric surgery, we isolated a strain that did not correspond to any

FIG. 1. Phylogenetic tree showing the position of '*Eisenbergiella massiliensis*' strain AT11 relative to other phylogenetically related species. Sequences were aligned using CLUSTALW, and phylogenetic inferences were obtained using the maximum-likelihood method within the MEGA software. Numbers at the nodes depict bootstrap percentage values obtained by repeating the analysis 500 times to yield a consensus tree. The bootstrap values of at least 95% were retained. The scale bar indicates a 1% nucleotide sequence divergence.



spectrum could not be identified by our systematic matrix-assisted laser desorption-ionization time-of-flight mass spectrometry (MALDI-TOF-MS) screening on a Microflex spectrometer (Bruker Daltonics, Bremen, Germany) was identified by the 16S rRNA gene sequencing [4]. The 16S rRNA gene was sequenced using fD1-rP2 primers as previously described [5], using a 3130-XL sequencer (Applied Biosciences, Saint Aubin, France). It displays 97.7% sequence similarity with *Eisenbergiella tayi* strain B086562 (= LMG 27400 = DSM 26961 = ATCC BAA-2558), the phylogenetically nearest species with standing nomenclature (Fig. 1). This fact putatively classifies strain AT11 as a member of the genus *Eisenbergiella* within the *Lachnospiraceae* family in the phylum *Firmicutes*. However, this percentage remains lower than the 98.7% 16S rRNA gene sequence threshold recommended by Stackebrandt and Ebers to delineate a new species [6]. Strain AT11 exhibited a 16S rRNA sequence divergence of 2.24% with its phylogenetically closest species with standing in nomenclature [7]. The strain AT11 was catalase-positive and oxidase-negative. Cells are Gram-negative staining, non-motile, non-spore-forming with a mean diameter of 2 µm by electron microscopy. Based on phenotypic and phylogenetic characteristics we propose the creation of a new species named '*Eisenbergiella massiliensis*' (ma.si.li.en'.sis. L. fem. adj. *massiliensis*, of Massilia, the Latin name of Marseille where '*Eisenbergiella massiliensis*' was first isolated). Strain AT11 is the type strain of the new species '*Eisenbergiella massiliensis*'.

MALDITOF-MS Spectrum Accession Number

The MALDITOF-MS spectrum of this strain is available at <http://www.mediterranee-infection.com/article.php?laref=256&titre=urms-database>.

Nucleotide Sequence Accession Number

The 16S rRNA gene sequence was deposited in GenBank under Accession number LN881600.

Deposit in a Culture Collection

Strain AT11 was deposited in the Collection de Souches de l'Unité des Rickettsies (CSUR) under number P2120.

Conflicts of Interest

No conflict of interest to declare.

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